

1655

Does Not Comply  
Corrected Diskette Needed

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/554,451

DATE: 05/07/2001  
TIME: 17:59:48

Input Set : A:\09554451.txt  
Output Set: N:\CRF3\05072001\I554451.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:  
5 (i) APPLICANT: *Response should be on same line as the heading.*  
6 Jonathan Paul MURPHY  
7 Anthony ATKINSON  
9 (ii) TITLE OF INVENTION: Detection of Molecules in Samples  
11 (iii) NUMBER OF SEQUENCES: 9  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: Pillsbury Winthrop, L.L.P.  
15 (B) STREET: 1100 New York Ave., N.W.  
16 (C) CITY: Washington  
17 (D) STATE: D.C.  
18 (E) COUNTRY: U.S.A.  
C--> 19 (F) ZIP: 20005  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Diskette  
23 (B) COMPUTER: IBM PC compatible  
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: MS Word  
27 (vi) CURRENT APPLICATION DATA:  
C--> 28 (A) APPLICATION NUMBER: US/09/554,451  
C--> 29 (B) FILING DATE: 15-May-2000  
30 (C) CLASSIFICATION:  
36 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER: PCT/GB98/03449  
34 (B) FILING DATE: November 16, 1998  
37 (A) APPLICATION NUMBER: GB 9723955.2  
38 (B) FILING DATE: November 14, 1997  
41 (2) INFORMATION FOR SEQ ID NO: 1:  
43 (i) SEQUENCE CHARACTERISTICS:  
44 (A) LENGTH: 191 amino acids  
45 (B) TYPE: amino acid  
46 (C) STRANDEDNESS: single  
47 (D) TOPOLOGY: linear  
49 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
51 Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg  
52 1 5 10 15  
54 Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu  
55 20 25 30  
57 Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro  
58 35 40 45  
60 Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg  
61 50 55 60  
63 Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu  
64 65 70 75 80  
66 Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val  
67 85 90 95

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```

69   Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp
71           100           105           110
73   Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu
74           115           120           125
76   Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Pro Lys Gln Thr Tyr Ser
77           130           135           140
79   Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
80           145           150           155           160
82   Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe
83           165           170           175
85   Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
86           180           185           190
89 (2) INFORMATION FOR SEQ ID NO: 2:
91   (i) SEQUENCE CHARACTERISTICS:
92       (A) LENGTH: 695 base pairs
93       (B) TYPE: nucleic acid
94       (C) STRANDEDNESS: single
95       (D) TOPOLOGY: linear
97   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
99 GGATCCTTTT TGTTTAACTT TAAGAAGGAG ATATACATAT GCGTCCGTCT ATCCACCGTA      60
101 CCGCTATCGC TGCTGTTCTG GCTACCGCTT TCGTTGCTGG TACCGCTCTG GCATTCCCGA      120
103 CCATCCCGCT GTCTCGTCTG TTCGACAACG CTATGCTGCG TGCTCACCGT CTGCACCAGC      180
105 TGGCTTTCGA CACCTACCAG GAATGGGAAG AAGCTTACAT CCCGAAAGAA CAGAAATACT      240
107 CTTTCCTGCA GAACCCGCAG ACCTCTCTGT GCTTCTCTGA ATCTATCCCG ACCCCGTCTA      300
109 ACCGTGAAGA AACCAGCAG AAATCTAACC TGGAAGTCTG GCGTATCTCT CTGCTGCTGA      360
111 TCCAGTCTTG GCTGGAACCG GTTCAGTTCC TGCGTTCTGT TTGGGCTAAC TCTCTGGTTT      420
113 ACGGTGCTTC TGA CTCTAAC GTTTACGACC TGCTGAAAGA CCTGGAAGAA GGTATCCAGA      480
115 CCCTGATGGG TCGTCTGGAA GACGGTTCTC CGCGTACCGG TCAGATCTTC AAACAGACCT      540
117 ACTCTAAATT CGACACCAAC TCTCACAACG ACGACGCTCT GCTGAAAAAC TACGGTCTGC      600
119 TGTACTGCTT CCGTAAAGAC ATGGACAAAG TTGAAACCTT CCTGCGTATC GTTCAGTGCC      660
121 GTTCTGTTGA AGGTTCTTGC GGTTCCTAAC TCGAG      695
124 (2) INFORMATION FOR SEQ ID NO: 3:
127   (i) SEQUENCE CHARACTERISTICS:
128       (A) LENGTH: 191 amino acids
129       (B) TYPE: amino acid
130       (C) STRANDEDNESS: single
131       (D) TOPOLOGY: linear
133   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
135   Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
136       1           5           10           15
138   Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Trp Glu
139       20           25           30
141   Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
142       35           40           45
144   Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg
145       50           55           60
147   Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Arg Ile Ser Leu
148       65           70           75           80
150   Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val

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```

151          85          90          95
153      Trp Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp
154          100          105          110
156      Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu
157          115          120          125
159      Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Pro Lys Gln Thr Tyr Ser
160          130          135          140
162      Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
163          145          150          155          160
165      Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe
166          165          170          175
168      Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
169          180          185          190

```

172 (2) INFORMATION FOR SEQ ID NO: 4:

174 (i) SEQUENCE CHARACTERISTICS:

175 (A) LENGTH: 32 amino acids

176 (B) TYPE: amino acid

177 (C) STRANDEDNESS: single

178 (D) TOPOLOGY: linear

180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

183      Cys Gly Asn Leu Ser Thr Cys Met Leu Gly Thr Tyr Thr Gln Asp Phe
184          1          5          10          15
186      Asn Lys Phe His Thr Phe Pro Gln Thr Ala Ile Gly Val Gly Ala Pro
187          20          25          30

```

190 (2) INFORMATION FOR SEQ ID NO: 5:

192 (i) SEQUENCE CHARACTERISTICS:

193 (A) LENGTH: 44 amino acids

194 (B) TYPE: amino acid

195 (C) STRANDEDNESS: single

196 (D) TOPOLOGY: linear

198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

200      Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
201          1          5          10          15
203      Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
204          20          25          30
206      Glu Ser Asn Gln Glu Arg Gly Ala Arg Arg Arg Leu
207          35          40

```

210 (2) INFORMATION FOR SEQ ID NO: 6:

212 (i) SEQUENCE CHARACTERISTICS:

213 (A) LENGTH: 21 amino acids

214 (B) TYPE: amino acid

215 (C) STRANDEDNESS: single

216 (D) TOPOLOGY: linear

218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

220      Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
221          1          5          10          15
223      Glu Asn Tyr Cys Asn
224          20

```

227 (2) INFORMATION FOR SEQ ID NO: 7:

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```

229      (i) SEQUENCE CHARACTERISTICS:
230          (A) LENGTH: 30 amino acids
231          (B) TYPE: amino acid
232          (C) STRANDEDNESS: single
233          (D) TOPOLOGY: linear
235      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
238      Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
239      1          5          10          15
241      Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
242      20          25          30
245 (2) INFORMATION FOR SEQ ID NO: 8:
247      (i) SEQUENCE CHARACTERISTICS:
248          (A) LENGTH: 165 amino acids
249          (B) TYPE: amino acid
250          (C) STRANDEDNESS: single
251          (D) TOPOLOGY: linear
253      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
255      Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Gln Arg Tyr Leu
256      1          5          10          15
258      Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
259      20          25          30
261      Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
262      35          40          45
264      Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
265      50          55          60
267      Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
268      65          70          75          80
270      Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
271      85          90          95
273      Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
274      100         105         110
276      Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
277      115         120         125
279      Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
280      130         135         140
282      Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
283      145         150         155         160
285      Cys Arg Thr Gly Asp
286      165
289 (2) INFORMATION FOR SEQ ID NO: 9:
291      (i) SEQUENCE CHARACTERISTICS:
292          (A) LENGTH: 133 amino acids
293          (B) TYPE: amino acid
294          (C) STRANDEDNESS: single
295          (D) TOPOLOGY: linear
297      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
299      Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
300      1          5          10          15
302      Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys

```

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```

303          20          25          30
305 Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
306          35          40          45
308 Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
309          50          55          60
311 Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
312          65          70          75          80
314 Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
315          85          90          95
317 Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
318          100          105          110
320 Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
321          115          120          125
323 Ile Ser Thr Leu Thr
324          130

```

VERIFICATION SUMMARY

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L:19 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]